

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 16, 2003, 16:37:55 : Search time 1447.31 Seconds
(without alignments)
15778.007 Million cell updates/sec

Title: US-09-497-967-44
Perfect score: 1410
Sequence: 1 atgaaaaataatttttagt.....cttattattattatgatga 1410

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16134066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	208.6	14.8	658	14 BQ135057	BQ135057 INIT1_2_G
C 2	205.2	14.6	607	14 BQ134912	BQ134912 INIT1_1_F
C 3	198	14.0	602	14 BQ135164	BQ135164 INIT1_4_B
C 4	197	14.0	590	14 BQ135179	BQ135179 INIT1_4_C
C 5	171	12.1	502	14 BQ134889	BQ134889 INIT1_1_D
C 6	163	11.6	445	14 BQ134871	BQ134871 INIT1_1_B

C 7	156.8	11.1	419	14 BQ135036	BQ135036 INIT1_2_D
C 8	134.4	9.5	675	14 BQ135196	BQ135196 INIT1_4_E
C 9	127.8	9.1	599	14 BQ134821	BQ134821 INIT1_4_D
C 10	115.2	8.2	540	14 BQ134879	BQ134879 INIT1_1_C
C 11	113.8	8.1	538	14 BQ134810	BQ134810 INIT1_4_C
C 12	110.4	7.8	630	14 BQ134905	BQ134905 INIT1_4_C
C 13	110.4	7.8	631	14 BQ134827	BQ134827 INIT1_1_F
C 14	109.4	7.8	523	14 BQ134970	BQ134970 INIT1_4_E
C 15	108.6	7.7	337	14 BQ134748	BQ134748 INIT1_2_D
C 16	106.4	7.5	514	14 BQ134761	BQ134761 INIT1_3_E
C 17	106.4	7.5	661	14 BQ135189	BQ135189 INIT1_3_F
C 18	105.8	7.5	560	14 BQ135129	BQ135129 INIT1_4_D
C 19	105.8	7.5	622	14 BQ134798	BQ134798 INIT1_3_F
C 20	105.8	7.5	687	14 BQ135168	BQ135168 INIT1_4_B
C 21	99.2	7.0	592	14 BQ134985	BQ134985 INIT1_2_G
C 22	72.2	5.1	210	14 BQ134900	BQ134900 INIT1_1_E
C 23	69.8	5.0	150	14 BQ135114	BQ135114 INIT1_3_E
C 24	68.4	4.9	773	17 CNS01VTC	AL169549 Tetraodon
C 25	62	4.4	735	17 CNS04NSM	AL299119 Tetraodon
C 26	61.4	4.4	470	17 FR0018463	AL011359 F.rubripe
C 27	61.4	4.4	989	17 CNS02HA4	AL197365 Tetraodon
C 28	61.4	4.4	1101	17 CNS0039G	AL063921 Drosophil
C 29	60.8	4.3	501	17 FR0048173	AL444958 Fugu rubr
C 30	58.4	4.1	605	17 AZ640388	AZ640388 1M0502E21
C 31	57.8	4.1	813	13 BJ406459	BJ406459 BJ406459
C 32	56.2	4.0	494	17 FR0048073	AL444858 Fugu rubr
C 33	56.2	4.0	572	17 CNS043SN	AL273200 Tetraodon
C 34	56.2	4.0	723	17 BH182027	BH182027 020_K_19-
C 35	56.2	4.0	723	17 CNS07NIN	AL618977 T3 end of
C 36	56	4.0	824	17 AZ185454	AZ185454 SP.1005_A
C 37	56	4.0	898	17 CNS04ALV	AL282028 Tetraodon
C 38	55.6	3.9	450	17 FR0025583	AL018519 F.rubripe
C 39	55.4	3.9	623	9 AU060774	AU060774 AU060774
C 40	55.4	3.9	742	9 AU060168	AU060168 AU060168
C 41	55	3.9	619	17 PR0006944	Z90754 F.rubripes
C 42	55	3.9	805	17 CNS04RW2	AL304427 Tetraodon
C 43	55	3.9	857	13 BJ403229	BJ403229 BJ403229
C 44	55	3.9	1101	17 CNS0039G	AL063921 Drosophil
C 45	54.8	3.9	550	17 FR0043207	AL130699 Fugu rubr

ALIGNMENTS

RESULT 1
BQ135057/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT

BQ135057 658 bp mRNA linear EST 22-APR-2002
INIT1_2_G01.g1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.

BQ135057
EST.
GI:20261156
Ichthyophthirius multifiliis.
Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligophenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
1 (bases 1 to 658)
Clark, I., Cordonnier-Pratt, M.-M., Sudman, M., Wentzel, V., Gingle, A.,
Dickerson, H., Lin, T.-L. and Pratt, L.H.
An EST database for Ichthyophthirius multifiliis (G5 isolate)
Unpublished (2002)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 67

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High quality sequence stop: 658
POLYA-No. Location/Qualifiers
1. .658
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 215 a 122 g 199 t
ORIGIN
Query Match 14.8%; Score 208.6; DB 14; Length 658;
Best Local Similarity 65.2%; Pred. No. 2.1e-34;
Matches 393; Conservative 0; Mismatches 189; Indels 21; Gaps 5;
QY 819 TCCTAATTCATCCAGGTAATAGTACATGCCTACCTGCCAGCAATAAAGATTAAGG 878
Db 604 TCCTATGGTTCCCTGGCCCTAATAGTAATCGGTAGCTTCGGAATCAAAAAGACCA-- 548
QY 879 TCGTGAGCCACTGCAGGTGGTCCGCTACTTTAGCCAAATAATGTAATATTCATGCC 938
Db 547 TCTTAATCCAGATCAGGCTCTTGGAGCTAATTTAGCCGATATGTGGCAGCTGAATGCC 488
QY 939 TGATGTACTGCAATTCGCTAGTGGAG---CAACTAATTAATTAATAAACAAGATG 995
Db 487 TGCTGACACTCTGTTACAGACGGAGTAACACCTACTTATCTGATCATCTCTCAATG 428
QY 996 TCTAATTTGCTGCTAACTTTATTTGATGTAATAATTTCTAGCGAGGAGTAGTAG 1055
Db 427 TGTAAATGTAAAGCTGGCTTTTACT---AAAATAGTAATTTTGAAGCAGGTAAGA 371
QY 1056 ATGCAAGCATGCCAGCAATAAAGTTTAAAGCGCTGTAGCAACTGCGAGGTGCTGC 1115
Db 370 ATGCATAAGTGTGCAGTAAGTAANAAGT---GGTTCAGCATCTGTTCCAGGTAATAGTGC 314
QY 1116 TACTTTAATTCGAATATGTCCTTGAATGCCCTGCTGTGCTAGTACTCACCGATGGAAC 1175
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QY 1176 AACATCTACTTAATAAAGCAGCATCTGAATGTTTAAATGCTGCCAAGCTTTTATAC 1235
Db 253 ATCAACTAATTTGTAGCTTTAGCAAGTGAATGTAATAATGTTAGGCTAATTTATGC 194
QY 1236 TACAAAATAAAGTATGGGTAGCAGGTAATGATACATGCTACTAGTGTGTAATAAATAAT 1295
Db 193 ATCAAAAACATCTGTTTTCAGCAGGTACTGATACATGCTACTGTAATGTTCTAAAAAAT 134
QY 1296 AACTTCGGCGCTGAAGCTAATTTACCTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1351
Db 133 AACTTCGGTGTACAGCTAAGTATATGCTGAAGTACTTAAAGAGCATAATGCGCCAG 74
QY 1352 -----ATTTCGCTAAATTTTATCAATTTCTTATTTATTTATTTATTTATTTATG 1406
Db 73 TTCACCTTTCCCAAAATTTTATCAATGCTCTTAATTTATTTATTTATTTATTTG 14
QY 1407 ATG 1409
Db 13 ATG 11
RESULT 2
BQ134912/c 607 bp mRNA linear EST 22-APR-2002
LOCUS
DEFINITION INIT1.1.F12.b1_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION BQ134912
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VERSION BQ134912.1 GI:20261011
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 607)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 599
POLYA-No. Location/Qualifiers
1. .607
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 199 a 111 c 104 g 193 t
ORIGIN
Query Match 14.6%; Score 205.2; DB 14; Length 607;
Best Local Similarity 65.8%; Pred. No. 1.1e-33;
Matches 383; Conservative 0; Mismatches 178; Indels 21; Gaps 5;
QY 841 ACTACATGCCCTACCTTGGCCAGCAATAAAGATTTATGTGCTGAAGCCACTGCGAGGTGGT 900
Db 607 AGTAAATCGTAGCTTGGCAATCAAAAAGACCAA---TTCCTAATCAGATCAGGTCTT 551
QY 901 GCGCTACTTTAGCCAAATAATGTAATTTGCATGCCCTGATGGTACTGCAATTTGCTAGT 960
Db 550 GAGGCTAATTTAGCCGATATATGGCACTGAATGCTCTGCTGGCAGCTTTGTTACAGAC 491
QY 961 GGAGCAA---CTAATTTATGTAATATTAACAGAAATGCTAAATTTGCTGCTAACTTT 1017
Db 490 GGAGTAACACCTTACTTATCTGATCTCATATAATGTTAATTTGTAAGCTGGCTTT 431
QY 1018 TATTTTGATGGTAATAATTTCTAGCAGGAGTAGTAGTCAAGAGCATGCTCCAGCAAT 1077
Db 430 TACT---AAAATAGTAATTTTGAAGCAGGTAAGGTTAATGCAATAAGTGTGCAGTAGT 374
QY 1078 AAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGCTACTTTTAAATTTGCATAATG 1137
Db 373 AAAACT---GGTTCAGCATCTGTTCCAGTAATAGTGTACTTTCAGGCACATAATGTTAA 317
QY 1138 CTTGAATGCCCTGCTGCTACTGCTACTCAGGATGGAACAACATCTACTTATAAATAAGCA 1197
Db 316 AACGATTTGCCCTGCTGGTACAGTGGTTGATGATGATCACTCACTTAATTTTGTAGCTTTA 257
QY 1198 GCATCTGAATGTTAAATGTGCTGCCAACTTTTATCTACAAAATAAACTGATTGGGTA 1257
Db 256 GCAAGTGAATGTAATAATTTAGCTACTTTTATGATCAAAACATCTGCTGTTTGA 197
QY 1258 GCAGGTATTTATACATGTAATAGTTTGTATAAATAAATAAATTAACCTTTCGGCCTGAAGCTAAT 1317
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D	b	479		CTGGCTTTTACTAAAA---TAGTAATTCGGAAGCAGGTAAAAAGTTAAATGCAATAAGTG TG	423
Q	y	1070	CAGCAAAATAAAGTTTTAAGCGCGTAGCAAC TGCAGGTGGTACTGCTACTCTTTTAATTGCC AT	1129	
D	b	422	CAGTAAGTAAA ACT ---GGTTCAGCATCTGTTCCAGGTAATAGTGCTACTTC GAGCCACAT	366	
Q	y	1130	AATGTGCGCCTTTGAATGCGCCTGCTGCTACTG TACTCACCGCATGGAACAACATCTACTTTATA	1189	
D	b	365	AATGTTAAAACGATGCGCCCTGCTGCTACAGTGT GGATGATGATGATCACTAAATTTTG	306	
Q	y	1190	AATAAGCAGCATCGAATGTGTTAAATGTGTCGCC AACATTTTATCTACAAAAATAAAC TG	1249	
D	b	305	TAGCTTTTACGAAGTGAATGCTACTAAATGT TAGCCFAACTTTTATGCATCAAAGAATCTG	246	
Q	y	1250	ATTGGGTAGCAGGTAATTCATACATGCTACTAG TTGTGAATAAAAAAATTAACTTCGCGCGTG	1309	
D	b	245	GTTTTCGACGAGGTACTGATCATGCTACTGAA TGTTCTAAAAANAATTAAC TTCGTGGTGTA	186	
Q	y	1310	AAGCTAATTTACCCTGAATCTGCTAAAAAATA TAATATGTG-----ATTTTCGGTA	1360	
D	b	185	CAGCTAAGATATATGCTGAAGCTACTTAAAG AAGCATATGCGCCAGTTCCTACTTCGCAA	126	
Q	y	1361	ATTTTATCAATTCCTTATTATTAATGATTTCTT ATTATTAATATGATGA	1410	
D	b	125	AATTTTATCAATGCTTAAATTAATTTCTTCTTA TTCTTCTTATTTGTTGATGA	76	
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L	O	CUS	BQ135179	590 bp mRNA linear EST 22-APR-2003	
D	E	F	INITI_4_C08_g1_A006_G5 trophont cDNA (INITI)	Ichthyophthirius multifiliis cDNA, mRNA sequence.	
A	C	S	BQ135179		
V	R	N	BQ135179.1 GI:20261278		
K	E	I	EST.		
S	O	R	Ichthyophthirius multifiliis.		
O	R	G	Ichthyophthirius multifiliis		
R	E	F	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;		
A	U	H	Hymenostomatida; Ophryoglenina; Ichthyophthirius.		
R	E	F	1 (bases 1 to 590)		
A	U	H	Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A., Dickerson,H., Lin,F.-L. and Pratt,L.H.		
J	O	N	An EST database for Ichthyophthirius multifiliis (G5 isolate) Unpublished (2002)		
C	M	N	Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu		
Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20.					
Seq primer: T7					
High quality sequence start: 43					
High quality sequence stop: 590					
POLYA=No.					
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			/strain="G5"		
			/db_xref="taxon:5932"		
			/clone_lib="G5 trophont cDNA (INTI1)"		
			/note="vector: pBluescript SK(-) from Lambda zap II; Site_1: EcoRI; Site_2: EcoRI. The library was made from trophont polyA+ RNA of the G5 parasite strain. Double-stranded cDNA was linked to EcoRI adaptors, size fractionated, and material >500 bp cloned into lambda Zap II. Plasmid DNA for sequencing was prepared by mass excision."		
B	A	S	207 a	94 g	186 t
O	R	I	c		

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Query Match      14.0%; Score 197; DB 14; Length 590;
Best Local Similarity 66.4%; Pred. No. 6.3e-32;
Matches 351; Conservative 0; Mismatches 160; Indels 18; Gaps 4;

QY 894 AGGTGGTGGCGTACTTTAGCCAAATAATAGTAATTTGTCAGTCCCTGATGGTACTGCAAT 953
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Db 590 AGGTCTTGAGGCTAATTTAGCGCATAATGTGGCACTGAATGCTCTGCTGGCACTCTTGT 531

QY 954 TGCTAGTCGAGCAA---CTAATATGTAATATTAACACAGAATGCTAAATTTGCTGC 1010
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Db 530 TACAGACGAGTAACACCTTACTATATCTATGTCATCTCTCATATGTTAATTTGAAGC 471

QY 1011 TAACTTTTTATTTTGTGTAATAATTTCTAGCGGAAGTAGTAGTCAAGCATGTCC 1070
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 470 TGGCTTTTACTAAA---TAGTAATTTGCAAGCAGGTAAGAGTTAATGCAATAGTGTGC 414

QY 1071 AGCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGCTACTTTAATTTGCATA 1130
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 413 AGTAAGTAAAACT---GGTTCAGCATCTGTTCCAGGTAATAGTGTACTTTCAGCCACATA 357

QY 1131 ATGTGCGCTTGAATGCCGCTGCTGCTACTACCGCATGCAACACATCTACTATAA 1190
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Db 356 ATGTTAAACAGATGCGCTGCTGGTACAGTGGTTGATGATGTACATCAACTAATTTTGT 297

QY 1191 ATAAGCAGCATCTGAATGTGTTAAATGTGCTGCCAACTTTTATATACTACAAATAAAGCTGA 1250
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Db 296 AGCTTTAGCAAGTAATGACTAATAATGTTAGGCTAACTTTTATGATCATCAAAAACATCTGG 237

QY 1251 TTGGGTAGCAGGATTTGATACATGACTAGTTGTAATTAATAAATTAAGTCTTGGCGCTGA 1310
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Db 236 TTTTGCAGCAGGTACTGATACATGACTGAATGTTCTAAAAAATTAAGTCTTGGTGTCTAC 177

QY 1311 AGCTAATTTACCTGAATCTGCTAAAAAAATATAATGTG-----ATTTGCGCTAA 1361
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Db 176 AGCTAAGTATATGCTGAAGCTACTTAAAGACATAATGCGCGACTTCCACTTTCGCAAA 117

QY 1362 TTTTATCAATTTCTTATTTATTTATTTCTTATTTATTTATTTATGATGA 1410
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Db 116 ATTTTATCAATGCTCTTAATTTATTTCTTCTTATTTGTTGTGATGA 68

RESULT 5
BQ134889/c      502 bp      mRNA      linear      EST 22-APR-2002
LOCUS
DEFINITION      IN111_L_D07.b1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cdna, mRNA sequence.
ACCESSION      BQ134889
VERSION        BQ134889.1 GI:20260988
KEYWORDS       EST.
SOURCE         Ichthyophthirius multifiliis.
ORGANISM       Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE      1 (bases 1 to 502)
AUTHORS        Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE          An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Cordonnier-pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 474
POLYA=yes.
Location/Qualifiers

FEATURES
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source          1. 502
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda Zap
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT      185 a      80 c      70 g      167 t
ORIGIN
Query Match      12.1%; Score 171; DB 14; Length 502;
Best Local Similarity 67.5%; Pred. No. 2.2e-26;
Matches 291; Conservative 0; Mismatches 125; Indels 15; Gaps 3;

QY 989 CAGAATGCTAAATGTGCTGCTAACTTTTATTTTGTAGTGAATAATTTCTAGCGAGAA 1048
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 498 CATAATGTGTTAATGTAAAGCTGGCTTTTACT---AAAATAGTAAATTCGAAGCAGGTA 442

QY 1049 GTAGTAGATGCAAGCATGTCACGCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTG 1108
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 441 AAAGTTAATGCAATAGAGTGCAGTAAGTAAACT---GGTTCAGCATCTGTTCCAGGTA 385

QY 1109 GTACTGCTACTTTAATTTGCATATGTCCTTGAATGCCCTGCTGGTACTGCTACTCACCG 1168
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 384 ATAGTGTACTTTCAGCCACATAATGTTAAACGATTCCTGCTGGTACAGTGGTTGATG 325

QY 1169 ATGGAACAACATCTACTTTATAATAAGCAGCATCTGAATGTGTTAAATGTGTCGCCAAT 1228
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 324 ATGTATCATCACTAAATTTTGTAGCTTTAGCAAGTGAATGACTAAATGTTAGGCTAACT 265

QY 1229 TTTTACTACAAATAAAGCTGATTGGCTAGCAGTATTTGATACATGACTAGTTGTAATA 1288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 264 TTTATGATCAAAACATCTGGTTTTCAGCAGGACTGATACATGACTGAATGTTCTA 205

QY 1289 AAAAATTAACCTTCGCGCTGAAGCTAATTTACCTGAATCTGCTAAAAAATAATAAT 1348
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Db 204 AAAAATTAACCTTCGCTGCTACAGCTAAAGTATATGCTGAAGCTACTTAAAAAGCAATA 145

QY 1349 GTG-----ATTTCGCTAAATTTTATCAATTTCTTATTTATTTATTTATTTATT 1399
    || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 GCGCAGTTCACATTCGCAAAATTTTATCAATGCTCTTAATTTATTTATTTCTTTCTATT 85

QY 1400 TATTATGATGA 1410
    || ||||| |||||
Db 84 TGTGTGATGA 74

RESULT 6
BQ134871/c      445 bp      mRNA      linear      EST 22-APR-2002
LOCUS
DEFINITION      IN111_L_B05.b1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cdna, mRNA sequence.
ACCESSION      BQ134871
VERSION        BQ134871.1 GI:20260970
KEYWORDS       EST.
SOURCE         Ichthyophthirius multifiliis.
ORGANISM       Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE      1 (bases 1 to 445)
AUTHORS        Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE          An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
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ORGANISM *Ichthyophthirius multifiliis*

LOCUS	BQ135196	675 bp	mRNA	linear	EST 22-APR-
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DEFINITION INIT1.4.E06.g1.A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION BQ135196
VERSION BQ135196.1 GI:20261295
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 675)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: T7
High quality sequence start: 42
High quality sequence stop: 675
POLYA-No. Location/Qualifiers
FEATURES
source
1..675
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 216 a 126 c 127 g 206 t
ORIGIN
Query Match 9.5%; Score 134.4; DB 14; Length 675;
Best Local Similarity 63.3%; Pred. No. 1.4e-18;
Matches 291; Conservative 0; Mismatches 156; Indels 13; Gaps 5;
QY 819 TCCTAATTTCAATCCAGGTAATAGTACATGCTTACCTTGCCCGAGCAATAAAGATTATGG 878
DB 459 TCCTATGGTTCTCGGCCCTAATAGTAATGCTAGCTTGCAGTAACAAAAGACCAA--- 403
QY 879 TGTCTGAAGCCACTGCAGGTGGTGGCGCTACTTTAGCCAAATAATTAATTTGCATGCC 938
DB 402 TTCTTAATCCAGATCAGGTCCTTGAGGCTAATTTAGCCGATTAATGTGGCAGTGAATGCC 343
QY 939 TGATGTACTGCAATTCGTAGTGGAG---CAACTAATTATGTAATTAATAACAGAAATG 995
DB 342 TGTCTGCACCTCTGTTTACAGCGGAGTACACCTACTTATATCTGATCATCTCATATAG 283
QY 996 TCTAAATGTGCTGAACCTTTTATTTTGGATGCTAATAATTTCTAGGCGAGGAAGTAGTAG 1055
DB 282 TGTTAATTTGAAAGCTGGCTTTTACT---AAAATAGTAATTTTCGAAGCAGGTAAGTA 226
QY 1056 ATCCAAAGCATGTCACAGCAATAAAGTTTAAAGCGCTGTFAGCACTGCAGGTGGTACTGC 1115
DB 225 ATGCAATAAGTGGCAGTAGTAAGTAACACT---GGTTCAGCATCTGTTCCAGGTAATAGTGC 169
QY 1116 TACTTTTAATTCGATAATGTGCCCTTGAATGCCCTGCTGCTACTGTACTACCGAGTGAAC 1175
DB 168 TACTTCAGGCACATAATGTTAAACGATTGGCCCTGCTGCTGACAGTGGTTGATGATGTAC 109
QY 1176 AACATCTACTTAAATAAGCAGCATCTGAATGTGTTAATGTGCTGCCAACTTTTATAC 1235

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Db 108 ATCAACTAATTTTGTAGCTTTAGCAAGTGAATGACTAATAATGTAGGTAACCTTTATGC 49
QY 1236 TACAATAAATCACTGATTGGGTAG-CAGGTATTGATACATG 1274
Db 48 ATCAAAAACATCTGGTTTGCACCCAGGTACTGATACAG 9
RESULT 9
BQ134821/c
LOCUS BQ134821
DEFINITION INIT1.4.D09.bl.A006 G5 trophont cDNA (INIT1) Ichthyophthirius
multifiliis cDNA, mRNA sequence.
ACCESSION BQ134821
VERSION BQ134821.1 GI:20260920
KEYWORDS EST.
SOURCE Ichthyophthirius multifiliis.
ORGANISM Ichthyophthirius multifiliis
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Ophryoglenina; Ichthyophthirius.
REFERENCE 1 (bases 1 to 599)
AUTHORS Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
Dickerson,H., Lin,T.-L. and Pratt,L.H.
TITLE An EST database for Ichthyophthirius multifiliis (G5 isolate)
JOURNAL Unpublished (2002)
COMMENT Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector, and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 506
POLYA-No. Location/Qualifiers
FEATURES
source
1..599
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site_1: EcoRI; Site_2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."
BASE COUNT 191 a 113 c 111 g 183 t 1 others
ORIGIN
Query Match 9.1%; Score 127.8; DB 14; Length 599;
Best Local Similarity 62.8%; Pred. No. 3.6e-17;
Matches 268; Conservative 0; Mismatches 147; Indels 12; Gaps 4;
QY 819 TCCTAATTTCAATCCAGGTAATAGTACATGCTTACCTTGCCCGAGCAATAAAGATTATGG 878
DB 431 TCCATATGGTTCTCGGCCCTAATAGTAATGCTAGCTTGCAGTAACAAAAGACCAA--- 375
QY 879 TGCTGAAGCCACTGCAGGTGGTGGCGCTACTTTAGCCAAATAATGTAATTTGCATGCC 938
DB 374 TTCTTAATCCAGATCAGGTCCTTGAGGCTAATTTAGCCGATTAATGTGGCAGTGAATGCC 315
QY 939 TGATGGTACTGCAATTCGTAGTGGAG---CAACTAATTTATGTAATATATAACAGAAATG 995
DB 314 TGTGGGCACTCTGTTTACAGAGCGGAGTAACACCTACTTATCTATCTACTCTCATATG 255
QY 996 TCTAAATGTGCTGCTGAACCTTTTATTTTGGATGTTAAATTTCTTAGCAGGAAGTAGTAG 1055
DB 254 TGTTAATTTGTAAGCTGGCTTTTACT---AAAATAGTAATTTTCGAAGCAGGTAAGTA 198

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QY 1056 ATGCAAGCATGTCACCAATAAAGTTTAAAGCGCTGTAGCAACTGCAGGTGGTACTGC 1115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 197 ATGCAATAAGTGTGCAGTAAGTAAACT---GGTTGAGCATCTGTTCAGGTAATAGTGC 141
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1116 TACTTTAATTGCAATATGTCCTTGAATGCCCTGCTGGTACTACACCGCATGGAAC 1175
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 140 TACTTCAGCCACATAATGTTAAACAGATTGCCCTGCTGTACAGTGGTGTAGATGGTAC 81
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1176 ACATCTACTTAAATAAGCAGCATCTGAATGTGTTAAATGTCGTGCCAATTTTATAC 1235
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 ATCAACTAATTTTGTAGCTTTAGCAAGTGAATGTACTAAATGTTAGGTAACTTTATGC 21
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1236 TACAAAA 1242
      |||||
Db 20 ATCAAAA 14
      |||||

RESULT 10
BQ134879
LOCUS
DEFINITION
  INIT1_1_C04.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
  multifiliis cDNA, mRNA sequence.
ACCESSION
  BQ134879
VERSION
  BQ134879.1 GI:20260978
KEYWORDS
  EST.
SOURCE
  Ichthyophthirius multifiliis.
  Ichthyophthirius multifiliis.
  Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
  Hymenostomatida; Ophryoglenina; Ichthyophthirius.
  1 (bases 1 to 540)
  Dickerson,H., Lin,T.-L. and Pratt,L.H.
  Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
  An EST database for Ichthyophthirius multifiliis (G5 isolate)
  Unpublished (2002)
  Contact: Cordonnier-Pratt MM
  Laboratory for Genomics and Bioinformatics
  The University of Georgia, Department of Plant Biology
  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
  Tel: 706 542 1860
  Fax: 706 583 0210
  Email: mmpratt@uga.edu
  Sequences have been trimmed to exclude PolyA, vector, and regions
  below Phred quality 16. The threshold for highest quality sequence
  is 20.
  Seq primer: JEN REV
  High quality sequence stop: 449
  POLYA=No.
  Location/Qualifiers
    1..540
      /organism="Ichthyophthirius multifiliis"
      /strain="G5"
      /db_xref="taxon:5932"
      /clone_lib="G5 trophont cDNA (INIT1)"
      /note="Vector: pBluescript SK(-) from Lambda Zap II;
      Site_1: EcoRI; Site_2: EcoRI; The library was made from
      trophont polyA+ RNA of the G5 parasite strain.
      Double-stranded cDNA was linked to EcoRI adaptors, size
      fractionated, and material >500 bp cloned into lambda ZAP
      II. Plasmid DNA for sequencing was prepared by mass
      excision."
BASE COUNT 163 a 97 c 97 g 183 t
ORIGIN

Query Match 8.2%; Score 115.2; DB 14; Length 540;
Best Local Similarity 60.0%; Pred. No. 1.8e-14;
Matches 245; Conservative 0; Mismatches 133; Indels 30; Gaps 2;

QY 1 ATGAAAAATAATTTTACTAATATTTTTCATTATTATTCATTAATAATTAATAAATCT 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 33 ATGAAATTTAATATTTTAAATAATTTTGATTATTTCCCTATTATTATTAATGAATTAAGACT 92
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GCTAATTGCTCTGTGGAACTGAACACTAACACAGCCGGATAAGTTGATGATCTAGGAAC 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 93 GTTAATTTGCTTAATGGTCTGCAATTCGAATGGAATAATCTGATACAGGAGTGCAGAT 152
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 CTGCAAAATGTTGTTAATTTAGAAAAACATTTTATTATATAATAATGCTGCTGCT----- 174
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 153 ATAAATACTTGTACTCAITTCGTTAAAAACACTTTTACTTTAATGGTGGTAATCCCTGCAGGT 212
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 -----TTCGTTCTCTGCTGTAGCTGTACACCTTTGTCCATAA 213
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 213 CAGGCTCCTGGTGTACAATTCAGGTGTTAGTCACTGATGATGATGATGATGATGATGAT 272
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 214 AAAAAAGATGCTGGTGTACCAATCCAGTGTAGTCACTGATGATGATGATGATGATGATGAT 273
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 CAAAA---GCCGATTCTCAACACAGATAAGGTGATGATGATGATGATGATGATGATGAT 329
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 274 AACGTTAAATGCCCTGCTGCTACCGCAATTCAGGTGAGCAACAGATTATGACGCAATA 333
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 330 AGCAACTTATGCTCCGCTGGCACTGCACTTGAAGATGATGATGATGATGATGATGATGAT 389
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 334 ATCAGAGAATGTTTAAATTTAGATAATTAATTTTATAATGAAATGCT 381
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 390 CTCACATAATGTTAATGTAACCTAACTTTTACTTTTAAATGCTGCT 437
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 11
BQ134810
LOCUS
DEFINITION
  BQ134810
  INIT1_4_C08.bl_A006 G5 trophont cDNA (INIT1) Ichthyophthirius
  multifiliis cDNA, mRNA sequence.
ACCESSION
  BQ134810
VERSION
  BQ134810.1 GI:20260909
KEYWORDS
  EST.
SOURCE
  Ichthyophthirius multifiliis.
  Ichthyophthirius multifiliis.
  Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
  Hymenostomatida; Ophryoglenina; Ichthyophthirius.
  1 (bases 1 to 538)
  Clark,T., Cordonnier-Pratt,M.-M., Sudman,M., Wentzel,V., Gingle,A.,
  Dickerson,H., Lin,T.-L. and Pratt,L.H.
  An EST database for Ichthyophthirius multifiliis (G5 isolate)
  Unpublished (2002)
  Contact: Cordonnier-Pratt MM
  Laboratory for Genomics and Bioinformatics
  The University of Georgia, Department of Plant Biology
  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
  Tel: 706 542 1860
  Fax: 706 583 0210
  Email: mmpratt@uga.edu
  Sequences have been trimmed to exclude PolyA, vector, and regions
  below Phred quality 16. The threshold for highest quality sequence
  is 20.
  Seq primer: JEN REV
  High quality sequence stop: 531
  POLYA=No.
  Location/Qualifiers
    1..538
      /organism="Ichthyophthirius multifiliis"
      /strain="G5"
      /db_xref="taxon:5932"
      /clone_lib="G5 trophont cDNA (INIT1)"
      /note="Vector: pBluescript SK(-) from Lambda Zap II;
      Site_1: EcoRI; Site_2: EcoRI; The library was made from
      trophont polyA+ RNA of the G5 parasite strain.
      Double-stranded cDNA was linked to EcoRI adaptors, size
      fractionated, and material >500 bp cloned into lambda ZAP
      II. Plasmid DNA for sequencing was prepared by mass
      excision."

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BASE COUNT 155 a 101 c 106 g 175 t
ORIGIN

Query Match 8.1%; Score 113.8; DB 14; Length 538;
Best Local Similarity 59.2%; Pred. No. 3.5e-14;
Matches 234; Conservative 0; Mismatches 152; Indels 9; Gaps 2;

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below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV
High quality sequence start: 189
High quality sequence stop: 303
POLYA-No.

FEATURES

source
Location/Qualifiers
1..337
/organism="Ichthyophthirius multifiliis"
/strain="G5"
/db_xref="taxon:5932"
/clone_lib="G5 trophont cDNA (INIT1)"
/note="Vector: pBluescript SK(-) from Lambda Zap II;
Site 1: EcoRI; Site 2: EcoRI; The library was made from
trophont polyA+ RNA of the G5 parasite strain.
Double-stranded cDNA was linked to EcoRI adaptors, size
fractionated, and material >500 bp cloned into lambda ZAP
II. Plasmid DNA for sequencing was prepared by mass
excision."

BASE COUNT 126 a 53 c 49 g 109 t
ORIGIN

Query Match 7.7%; Score 108.6; DB 14; Length 337;
Best Local Similarity 68.5%; Pred. No. 4.6e-13;
Matches 183; Conservative 0; Mismatches 74; Indels 10; Gaps 2;
QY 1154 GTACTGTACTCACCAGTGAACACATCTACTTATAAATAAGCAGCATCTGAATGTGTTA 1213
||| | | ||| | | | | | | | | | | | | | | | | |
Db 337 GTACAGTGGTTGATGATGTCATCACTAATTTGTAGCTTTAGCAAGTGAATGACTA 278
QY 1214 AATGCTGCCAACHTTTATCTACAAATAAAGTATGGGTAGCAGGTTATGATACAT 1273
||| | | ||| | | | | | | | | | | | | | | | | |
Db 277 AATGTTAGGCTAACTTTATGCATCAAAACATCTGGTTTGCAGCAGGTACTGATACAT 218
QY 1274 GTAAT-AGTTGTAATAAAATTAACCTCTGCGCTGAAGCTAATTTACCTGAATCTGCT 1332
||| | | | | | | | | | | | | | | | | | | | | |
Db 217 GTACTGAATGTTCTTAAATAATTAACCTCTGCTGCTACAGCTAAAGTATATGCTGAAGCT 158
QY 1333 AAAAAAATATATATATG-ATTCGCTAATTTTATCAATTTTCCTTATTA 1383
| | | | | | | | | | | | | | | | | | | | | | | |
Db 157 ACTTAAAAAGCATATATGCCAGTTCACACTTTCGCATAATTTTATCAATGCTCCTTAATA 98
QY 1384 TTGATTTCTTATTTATTTATGATGA 1410
|| | | | | | | | | | | | | | | | | | | | | | |
Db 97 TTTATTCTTCTTATTTGTTGATGA 71

Search completed: February 16, 2003, 22:25:14
Job time : 1455.31 secs